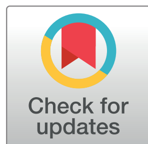
PLOS ONE

CORRECTION

Correction: Evidence for plant-derived xenomiRs based on a large-scale analysis of public small RNA sequencing data from human samples

Qi Zhao, Yuanning Liu, Ning Zhang, Menghan Hu, Hao Zhang, Trupti Joshi, Dong Xu



OPEN ACCESS

Citation: Zhao Q, Liu Y, Zhang N, Hu M, Zhang H, Joshi T, et al. (2020) Correction: Evidence for plant-derived xenomiRs based on a large-scale analysis of public small RNA sequencing data from human samples. PLoS ONE 15(3): e0230146. https://doi.org/10.1371/journal.pone.0230146

Published: March 11, 2020

Copyright: © 2020 Zhao et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

The references in the Correction notice do not provide direct support to the points made in the text. The authors have supplied updated references. An increasing number of studies have supported the xenomiR hypothesis in recent years. Li et al. [3] reported that continuous administration of a high plant miRNA diet or synthetic miR156 elevated miR156 levels and inhibited the Wnt/β-catenin signalling pathway in mouse intestine, and demonstrated that plant miR156 inhibits intestine cell proliferation by targeting Wnt10b. The same group also reported that miR167e-5p regulated the proliferation of enterocytes *in vitro* [4]. Hou et al. [5] showed that plant miR156a stably presents in healthy human serum. Their *in vitro* studies demonstrated that miR156a directly targeted the junction adhesion molecule-A, and ectopic expression of MiR156a in human aortic endothelial cells reduced inflammatory cytokine-induced monocytes adhesion by suppressing JAM-A. Moreover, in addition to the two studies mentioned in our paper [6; 7], one more study has shown that breast milk contains plant derived microRNAs (miR166a, miR156a, miR157a, miR172a, miR168a) and the concentration of these microRNAs were measured [8].

Not limited to mammals, plant-derived xenomiRs also exist and function in insects and bacteria. Zhu et al. [9] reported plant miRNAs miR162a in bee bread targeted amTOR in bees, which delayed development and decreased body and ovary size in honeybees, thereby preventing larval differentiation into queens and inducing development into worker bees. Another research suggested that exosome-like extracellular vesicles secreted from *Arabidopsis* cells transported small RNAs into the fungal pathogen *B. cinerea*, which suppressed its pathogenicity by silencing fungal virulence genes [10].

A number of studies have investigated plant derived xenomiRs using computational approaches. Patel et al. [11] identified conserved and novel *O. basilicum* miRNAs from expressed sequenced tags using computational approaches, and predicted their targets and potential functions on human. Using bioinformatics tools and databases, Ergün [12] investigated cross-kingdom gene regulation via miRNAs of *H. perforatum* flower dietetically absorbed to define potential biomarkers for prostate cancer. Yu et al. [13] developed a related database MepmiRDB, which collected thousands of potential miRNAs/xenomiRs belonging to 29 medicinal plant species. Zhao et al. [14] analyzed the differences between 166 plant-derived xenomiRs and 942 non-xenomiRs, and trained a 1D-CNN model to predicted other possible xenomiRs from unlabeled plant miRNA sequences.

These studies not only supported the xenomiR hypothesis from different approaches and species, but also started to explore the function, mechanism and medicinal value of plant derived xenomiRs. More related researches were well-reviewed in two recent papers [15, 16].

The authors would also clarify the type of t-test used in the comparison of abundance values of plant miRNAs in human samples (S5 Table) and those of human miRNAs in *Arabidopsis* samples (S8 Table). The authors state that they used "independent samples Student's t-test" when comparing abundances between the plant miRNA in human samples and human miRNAs in *Arabidopsis* samples. Here, the denary logarithm of plant miRNA abundances of human samples and human miRNAs of *Arabidopsis* samples were assumed to follow Gaussian distributions.

When the abundances of plant derived miRNAs in human samples were analyzed, only the top 24 most abundant plant miRNAs (S3 Table) with abundance more than 0.05 were used, which include most of the plant miRNAs reported by other studies. In many samples, the abundance values of these 24 types of miRNA were 0, and none of these were not excluded. For computational convenience, a very small pseudo-abundance was added to all abundance values (see the Materials and methods section in the original article [1]). The authors confirm the resulting p-values are correct except the p-value that was corrected in [2].

References

1. Zhao Q, Liu Y, Zhang N, Hu M, Zhang H, Joshi T, et al. (2018) Evidence for plant-derived xenomiRs based on a large-scale analysis of public small RNA sequencing data from human samples. PLoS ONE 13(6): e0187519. https://doi.org/10.1371/journal.pone.0187519 PMID: 29949574
2. Zhao Q, Liu Y, Zhang N, Hu M, Zhang H, et al. (2019) Correction: Evidence for plant-derived xenomiRs based on a large-scale analysis of public small RNA sequencing data from human samples. PLOS ONE 14(10): e0224537. https://doi.org/10.1371/journal.pone.0224537 PMID: 31648238
3. Li M, Chen T, Wang R, Luo JY, He JJ, Ye RS, et al. Plant MIR156 regulates intestinal growth in mammals by targeting the Wnt/beta-catenin pathway. Am J Physiol Cell Physiol. 2019; 317(3):C434–C48. Epub 2019/06/06. https://doi.org/10.1152/ajpcell.00030.2019 PMID: 31166713.
4. Li M, Chen T, He JJ, Wu JH, Luo JY, Ye RS, et al. Plant MIR167e-5p Inhibits Enterocyte Proliferation by Targeting beta-Catenin. Cells. 2019; 8(11). Epub 2019/11/07. https://doi.org/10.3390/cells8111385 PMID: 31689969.
5. Hou DX, He FF, Ma LN, Cao MH, Zhou Z, Wei Z, et al. The potential atheroprotective role of plant MIR156a as a repressor of monocyte recruitment on inflamed human endothelial cells. Journal of Nutritional Biochemistry. 2018; 57:197–205. https://doi.org/10.1016/j.jnutbio.2018.03.026 PMID: 29751293
6. Ma J, Wang C, Long K, Zhang H, Zhang J, Jin L, et al. Exosomal microRNAs in giant panda (Ailuropoda melanoleuca) breast milk: potential maternal regulators for the development of newborn cubs. Scientific reports. 2017; 7(1):3507. https://doi.org/10.1038/s41598-017-03707-8 PMID: 28615713
7. Baier SR, Nguyen C, Xie F, Wood JR, Zempleni J. Diet-Responsive Mammalian miRNAs Are Likely Endogenous Reply. J Nutr. 2014; 144(11):1881-.
8. Lukasik A, Brzozowska I, Zielenkiewicz U, Zielenkiewicz P. Detection of Plant miRNAs Abundance in Human Breast Milk. International Journal of Molecular Sciences. 2017; 19(1). https://doi.org/10.3390/ijms19010037 PMID: 29295476
9. Zhu K, Liu M, Fu Z, Zhou Z, Kong Y, Liang H, et al. Plant microRNAs in larval food regulate honeybee caste development. PLoS Genet. 2017; 13(8):e1006946. https://doi.org/10.1371/journal.pgen.1006946 PMID: 28859085
10. Cai Q, Qiao L, Wang M, He B, Lin FM, Palmquist J, et al. Plants send small RNAs in extracellular vesicles to fungal pathogen to silence virulence genes. Science. 2018. https://doi.org/10.1126/science.aar4142 PMID: 29773668.
11. Patel M, Mangukia N, Jha N, Gadhavi H, Shah K, Patel S, et al. Computational identification of miRNA and their cross kingdom targets from expressed sequence tags of Ocimum basilicum. Mol Biol Rep. 2019; 46(3):2979–95. Epub 2019/05/09. https://doi.org/10.1007/s11033-019-04759-x PMID: 31066002.
12. Ergün S. Cross-Kingdom Gene Regulation via miRNAs of Hypericum Perforatum (St. John's wort) Flower Dietetically Absorbed: An In Silico Approach to Define Potential Biomarkers for Prostate Cancer. Computational Biology and Chemistry. 2019.
13. Yu D, Lu J, Shao W, Ma X, Xie T, Ito H, et al. MepmiRDB: a medicinal plant microRNA database. Database (Oxford). 2019; 2019. Epub 2019/06/25. https://doi.org/10.1093/database/baz070 PMID: 31231773

14. Zhao Q, Mao Q, Zhao Z, Dou T, Wang Z, Cui X, et al. Prediction of plant-derived xenomiRs from plant miRNA sequences using random forest and one-dimensional convolutional neural network models. BMC Genomics. 2018; 19(1):839. https://doi.org/10.1186/s12864-018-5227-3 PMID: 30477446

15. Zhang L, Chen T, Yin Y, Zhang CY, Zhang YL. Dietary microRNA-A Novel Functional Component of Food. Adv Nutr. 2019; 10(4):711–21. Epub 2019/05/24. https://doi.org/10.1093/advances/nmy127 PMID: 31120095.

16. Zeng J, Gupta VK, Jiang Y, Yang B, Gong L, Zhu H. Cross-Kingdom Small RNAs Among Animals, Plants and Microbes. Cells. 2019; 8(4):371.